SEQUENCE LISTING

<110> Williamson, Mark

<120> MDA-9 AND USES THEREOF

<130> 07334-122001

<140> US 09/531,369
<141> 2000-03-21

<150> US 60/125,759
<151> 1999-03-23

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<170> FastSEQ for Windows Version 4.0

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                 Met Ser Leu Tyr Pro Ser Leu Glu Asp Leu Lys Val
                   1               5                  10

gac aaa gta att cag gct caa act gct ttt tct gca aac cct gcc aat      159
Asp Lys Val Ile Gln Ala Gln Thr Ala Phe Ser Ala Asn Pro Ala Asn
          15                  20                  25

cca gca att ttg tca gaa gct tct gct cct atc cct cac gat gga aat      207
Pro Ala Ile Leu Ser Glu Ala Ser Ala Pro Ile Pro His Asp Gly Asn
      30                  35                  40

ctc tat ccc aga ctg tat cca gag ctc tct caa tac atg ggg ctg agt      255
Leu Tyr Pro Arg Leu Tyr Pro Glu Leu Ser Gln Tyr Met Gly Leu Ser
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tta aat gaa gaa gaa ata cgt gca aat gtg gcc gtg gtt tct ggt gca      303
Leu Asn Glu Glu Glu Ile Arg Ala Asn Val Ala Val Val Ser Gly Ala
                 65                  70                  75

cca ctt cag ggg cag ttg gta gca aga cct tcc agt ata aac tat atg      351
Pro Leu Gln Gly Gln Leu Val Ala Arg Pro Ser Ser Ile Asn Tyr Met
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gtg gct cct gta act ggt aat gat gtt gga att cgt aga gca gaa att      399
Val Ala Pro Val Thr Gly Asn Asp Val Gly Ile Arg Arg Ala Glu Ile
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aag caa ggg att cgt gaa gtc att ttg tgt aag gat caa gat gga aaa      447
Lys Gln Gly Ile Arg Glu Val Ile Leu Cys Lys Asp Gln Asp Gly Lys
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att gga ctc agg ctt aaa tca ata gat aat ggt ata ttt gtt cag cta      495
Ile  ly Leu Arg Leu Lys Ser Ile Asp Asn Gly Ile Phe Val Gln Leu
125                 130                 135                 140

gtc cag gct aat tct cca gcc tca ttg gtt ggt ctg aga ttt ggg gac      543
Val Gln Ala Asn Ser Pro Ala Ser Leu Val Gly Leu Arg Phe Gly Asp
                145                 150                 155

caa gta ctt cag atc aat ggt gaa aac tgt gca gga tgg agc tct gat      591
Gln Val Leu Gln Ile Asn Gly Glu Asn Cys Ala Gly Trp Ser Ser Asp
            160                 165                 170

aaa gcg cac aag gtg ctc aaa cag gct ttt gga gag aag att acc atg      639
Lys Ala His Lys Val Leu Lys Gln Ala Phe Gly Glu Lys Ile Thr Met
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acc att cgt gac agg ccc ttt gaa cgg acg att acc atg cat aag gat      687
Thr Ile Arg Asp Arg Pro Phe Glu Arg Thr Ile Thr Met His Lys Asp
    190                 195                 200

agc act gga cat gtt ggt ttt atc ttt aaa aat gga aaa ata aca tcc      735
Ser Thr Gly His Val Gly Phe Ile Phe Lys Asn Gly Lys Ile Thr Ser
205                 210                 215                 220

ata gtg aaa gat agc tct gca gcc aga aat ggt ctt ctc acg gaa cat      783
Ile Val Lys Asp Ser Ser Ala Ala Arg Asn Gly Leu Leu Thr Glu His
                225                 230                 235

aac atc tgt gaa atc aat gga cag aat gtc att gga ttg aag gac tct      831
Asn Ile Cys Glu Ile Asn Gly Gln Asn Val Ile Gly Leu Lys Asp Ser
            240                 245                 250

caa att gca gac ata ctg tca aca tct ggg act gta gtt act att aca      879
Gln Ile Ala Asp Ile Leu Ser Thr Ser Gly Thr Val Val Thr Ile Thr
        255                 260                 265

atc atg cct gct ttt atc ttt gaa cat att att aag cgg atg gca cca      927
Ile Met Pro Ala Phe Ile Phe Glu His Ile Ile Lys Arg Met Ala Pro
    270                 275                 280

agc att atg aaa agc cta atg gac cac acc att cct gag gtt t            970
Ser Ile Met Lys Ser Leu Met Asp His Thr Ile Pro Glu Val
285                 290                 295

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35 40 45
Leu Tyr Pro Glu Leu Ser Gln Tyr Met Gly Leu Ser Leu Asn Glu Glu
50 55 60
Glu Ile Arg Ala Asn Val Ala Val Val Ser Gly Ala Pro Leu Gln Gly
65 70 75 80
Gln Leu Val Ala Arg Pro Ser Ser Ile Asn Tyr Met Val Ala Pro Val
85 90 95
Thr Gly Asn Asp Val Gly Ile Arg Arg Ala Glu Ile Lys Gln Gly Ile
100 105 110
Arg Glu Val Ile Leu Cys Lys Asp Gln Asp Gly Lys Ile Gly Leu Arg
115 120 125
Leu Lys Ser Ile Asp Asn Gly Ile Phe Val Gln Leu Val Gln Ala Asn
130 135 140
Ser Pro Ala Ser Leu Val Gly Leu Arg Phe Gly Asp Gln Val Leu Gln
145 150 155 160
Ile Asn Gly Glu Asn Cys Ala Gly Trp Ser Ser Asp Lys Ala His Lys
165 170 175
Val Leu Lys Gln Ala Phe Gly Glu Lys Ile Thr Met Thr Ile Arg Asp
180 185 190
Arg Pro Phe Glu Arg Thr Ile Thr Met His Lys Asp Ser Thr Gly His
195 200 205
Val Gly Phe Ile Phe Lys Asn Gly Lys Ile Thr Ser Ile Val Lys Asp
210 215 220
Ser Ser Ala Ala Arg Asn Gly Leu Leu Thr Glu His Asn Ile Cys Glu
225 230 235 240
Ile Asn Gly Gln Asn Val Ile Gly Leu Lys Asp Ser Gln Ile Ala Asp
245 250 255
Ile Leu Ser Thr Ser Gly Thr Val Val Thr Ile Thr Ile Met Pro Ala
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Ser Leu Met Asp His Thr Ile Pro Glu Val
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A1 CONCLUD


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